**THAT WHICH IS CLAIMED IS:**

1. A method of assessing the relationship between a poinsettia plant and a known poinsettia cultivar, the method comprising the steps of:

(a) obtaining a DNA fingerprint of the poinsettia plant's genomic DNA by AFLP, the fingerprint being a collection of amplified restriction fragments;

(b) comparing the fingerprint obtained in (a) with a genomic DNA fingerprint of the known poinsettia cultivar; and

(c) assessing the relationship between the plant and the cultivar by identifying the presence or absence of similarities between the fingerprints.

2. The method of Claim 1, wherein the fragments comprise DNA sequences that include DNA sequences selected from the group consisting of **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**.

3. A method of estimating a genetic relationship of a first poinsettia plant to a poinsettia plant that is a representative member of a specific breeding family, comprising:

(a) obtaining a DNA fingerprint of the genomic DNA of a first poinsettia plant by AFLP, wherein the fingerprint comprises a set of amplified restriction fragments;

(b) comparing the fingerprint of the first poinsettia plant with a fingerprint of the genomic DNA of the poinsettia plant that is a representative member of a specific breeding family, wherein the fingerprint comprises a set of amplified restriction fragments;

(c) generating a profile index value based on the comparison of the fingerprint of the first poinsettia plant with the fingerprint of the poinsettia plant that is a representative member of a specific breeding family, wherein a profile similarity index value of about one or a dissimilarity value of about zero indicates that the two poinsettia plants are representatives of the same breeding family.

4. The method of Claim 3, wherein each fragment comprises a DNA sequence that includes a DNA sequence selected from the group consisting of **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**.

5. The method of Claim 3, wherein the specific breeding family is selected from the group consisting of the Freedom, Peterstar, and Sonora cultivars.

6. The method according to Claim 3, wherein the AFLP analysis is carried out by first digesting the genomic DNA with a restriction enzyme that has a tetranucleotide recognition site and a restriction enzyme that has a hexanucleotide recognition site.

7. The method according to Claim 6, wherein the restriction enzyme that has a tetranucleotide recognition site is *Mse*I, and the restriction enzyme that has a hexanucleotide recognition site is *Eco*RI.

8. The method according to Claim 3, wherein the AFLP analysis is carried out using primers that contain sequences selected from the group consisting of **SEQ ID NO:47, SEQ ID NO: 48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53** and **SEQ ID NO:54.**

9. The method according to Claim 3, wherein the AFLP analysis is carried out using eight primer pairs, and wherein the eight primer pairs include primers of the sequence of **SEQ ID NO:47** and **SEQ ID NO:51**; **SEQ ID NO:47** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:51**; **SEQ ID NO: 48** and **SEQ ID NO:52**; **SEQ ID NO: 48** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:54**; **SEQ ID NO:49** and **SEQ ID NO:50**; or **SEQ ID NO:49** and **SEQ ID NO:51.**

10. The method of Claim 3, wherein the fingerprint of the genomic DNA of the first poinsettia plant is used to generate a profile of the poinsettia plant, wherein the profile comprises the number of restriction fragments that

correspond to DNA sequences that include the DNA sequences **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19**, **20, 21, 22, 23, 24**, **25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of the fragments; and wherein (b) comprises comparing the profile of the poinsettia plant to a profile generated from the fingerprint of the poinsettia plant that is a representative member of a specific breeding family, wherein the profile of the poinsettia plant that is a representative member of a specific breeding family comprises the number of restriction fragments that correspond to DNA sequences that include the DNA sequences **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19**, **20, 21, 22, 23, 24**, **25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of the fragments.

11. The method of Claim 10, wherein the profile of at least one of the first poinsettia plant and the profile of the poinsettia plant that is a representative member of a specific breeding family is stored in a database comprising profiles of known poinsettia plants, and wherein the profiles of the known poinsettia cultivars comprise the number of restriction fragments that correspond to DNA sequences that include the DNA sequences **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19**, **20, 21, 22, 23, 24**, **25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of the fragments.

12. A method of determining the profile similarity of a first plant to a second plant, comprising:

(a) obtaining a DNA fingerprint of the genomic DNA of a first plant by AFLP, wherein the fingerprint comprises a set of amplified restriction fragments and wherein each fragment comprises a DNA sequence that includes a DNA sequence selected from the group consisting of **SEQ ID NO**: **1** to **SEQ ID NO**: **46**;

(b) comparing the fingerprint of the first plant with a fingerprint of the genomic DNA of the second plant, wherein the fingerprint comprises a set of amplified restriction fragments and wherein each fragment comprises a DNA sequence that includes a DNA sequence selected from the group consisting of **SEQ ID NO**: **1** to **SEQ ID NO**: **46**; and

(c) generating a profile index value based on the comparison of the fingerprint of the first plant with the fingerprint of the second plant, wherein a

profile similarity index value of about 1 or a dissimilarity value of about zero indicates that the two plants are genetically similar.

13. The method according to Claim 12, wherein the AFLP analysis is carried out by first digesting the genomic DNA with a restriction enzyme that has a tetranucleotide recognition site and a restriction enzyme that has a hexanucleotide recognition site.

14. The method according to Claim 13 wherein the restriction enzyme that has a tetranucleotide recognition site is *Mse*I, and the restriction enzyme that has a hexanucleotide recognition site is *Eco*RI.

15. The method according to Claim 12, wherein the AFLP analysis is carried out using primers selected from the group consisting of sequences that include **SEQ ID NO:47, SEQ ID NO: 48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53** and **SEQ ID NO:54.**

16. The method according to Claim 12, wherein the AFLP analysis is carried out using eight primer pairs, and wherein the eight primer pairs include primers of the sequence of **SEQ ID NO:47** and **SEQ ID NO:51**; **SEQ ID NO:47** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:51**; **SEQ ID NO: 48** and **SEQ ID NO:52**; **SEQ ID NO: 48** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:54**; **SEQ ID NO:49** and **SEQ ID NO:50**; and **SEQ ID NO:49** and **SEQ ID NO:51.**

17. The method of Claim 12, wherein the fingerprint of the genomic DNA of the first plant is used to generate a profile of the plant, wherein the profile comprises the number of restriction fragments that correspond to DNA sequences that include the DNA sequences **SEQ ID NO: 1** to **SEQ ID NO: 46**, and the identity of the fragments; and wherein (b) comprises comparing the profile of the plant to a profile generated from the fingerprint of the second plant, wherein the profile of the second plant comprises the number of restriction fragments that correspond to DNA sequences that include the DNA

sequences **SEQ ID NO**: **1** to **SEQ ID NO**: **46**, and the identity of the fragments.

18. The method of Claim 17, wherein the profile of at least one of the first and the second plants is stored in a database comprising profiles of known cultivars, and wherein the profiles of the known cultivars comprise the number of restriction fragments that correspond to DNA sequences that include the DNA sequences **SEQ ID NO**: **1** to **SEQ ID NO**: **46**, and the identity of the fragments.

19. The method according to Claim 18, wherein the database is stored in a computer-readable storage medium.

20. The method according to Claim 12, wherein the comparing step is carried out by a computer.

21. A method of determining the profile similarity of a first poinsettia plant to a second poinsettia plant, comprising:

(a) obtaining a DNA fingerprint of the genomic DNA of a first poinsettia plant by AFLP, wherein the fingerprint comprises a set of amplified restriction fragments;

(b) comparing the fingerprint of the first poinsettia plant with a fingerprint of the genomic DNA of the second poinsettia plant, wherein the fingerprint comprises a set of amplified restriction fragments; and

(c) generating a profile index value based on the comparison of the fingerprint of the first poinsettia plant with the fingerprint of the second plant, wherein a profile similarity index value of about 1 or a dissimilarity value of about zero indicates that the two poinsettia plants are genetically similar.

22. The method according to Claim 21, wherein each fragment comprises a DNA sequence that includes a DNA sequence selected from the group consisting of **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**.

23. The method according to Claim 21, wherein the AFLP analysis is carried out by first digesting the genomic DNA with a restriction enzyme that has a tetranucleotide recognition site and a restriction enzyme that has a hexanucleotide recognition site.

24. The method according to Claim 23, wherein the restriction enzyme that has a tetranucleotide recognition site is *Mse*I, and the restriction enzyme that has a hexanucleotide recognition site is *Eco*RI.

25. The method according to Claim 21, wherein the AFLP analysis is carried out using primers selected from the group consisting of sequences that include **SEQ ID NO:47, SEQ ID NO: 48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53** and **SEQ ID NO:54.**

26. The method according to Claim 21, wherein the AFLP analysis is carried out using eight primer pairs, and wherein the eight primer pairs include primers of the sequence of **SEQ ID NO:47** and **SEQ ID NO:51**; **SEQ ID NO:47** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:51**; **SEQ ID NO: 48** and **SEQ ID NO:52**; **SEQ ID NO: 48** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:54**; **SEQ ID NO:49** and **SEQ ID NO:50**; and **SEQ ID NO:49** and **SEQ ID NO:51.**

27. The method of Claim 21, wherein the fingerprint of the genomic DNA of the first poinsettia plant is used to generate a profile of the poinsettia plant, wherein the profile comprises the number of restriction fragments that correspond to DNA sequences that include the DNA sequences **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of the fragments; and wherein (b) comprises comparing the profile of the poinsettia plant to a profile generated from the fingerprint of the second poinsettia plant, wherein the profile of the second poinsettia plant comprises the number of restriction fragments that correspond to DNA sequences that include the DNA sequences **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of the fragments.

28. The method of Claim 27, wherein the profile of at least one of the first and the second poinsettia plants is stored in a database comprising profiles of known poinsettia cultivars, and wherein the profiles of the known poinsettia cultivars comprise the number of restriction fragments that correspond to DNA sequences that include the DNA sequences **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of the fragments.

29. The method according to Claim 28, wherein the database is stored in a computer-readable storage medium.

30. The method according to Claim 21, wherein the comparing step is carried out by a computer.

31. A method of generating a profile of a poinsettia plant, wherein the profile comprises the number of amplified restriction fragments having a sequence that includes the sequence selected from the group consisting of **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of each fragment, comprising:

(a) obtaining a DNA fingerprint of the genomic DNA of the poinsettia plant, wherein the fingerprint is a set of amplified restriction fragments, and wherein each fragment comprises a DNA sequence that includes a DNA sequence selected from the group consisting of **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**;

(b) identifying the amplified restriction fragments having a sequence that includes a sequence selected from the group consisting of **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44** in the fingerprint; and

(c) recording the amplified restriction fragments having a sequence that includes a sequence selected from the group consisting of **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of each fragment.

32. The method according to Claim 31, wherein the DNA fingerprint of the genomic DNA of the poinsettia plant is obtained by AFLP analysis.

33. The method according to Claim 32, wherein the AFLP analysis is carried out by first digesting the genomic DNA with a restriction enzyme that has a tetranucleotide recognition site and a restriction enzyme that has a hexanucleotide recognition site.

34. The method according to Claim 33, wherein the restriction enzyme that has a tetranucleotide recognition site is *Mse*I, and the restriction enzyme that has a hexanucleotide recognition site is *Eco*RI.

35. The method according to Claim 32, wherein the AFLP analysis is carried out using primers that include sequences selected from the group consisting of **SEQ ID NO:47, SEQ ID NO: 48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53** and **SEQ ID NO:54.**

36. The method according to Claim 32, wherein the AFLP analysis is carried out using eight primer pairs, and wherein the eight primer pairs include primers of the sequence of **SEQ ID NO:47** and **SEQ ID NO:51**; **SEQ ID NO:47** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:51**; **SEQ ID NO: 48** and **SEQ ID NO:52**; **SEQ ID NO: 48** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:54**; **SEQ ID NO:49** and **SEQ ID NO:50**; and **SEQ ID NO:49** and **SEQ ID NO:51.**

37. The method according to Claim 31, wherein the profile is recorded into a database comprising at least one other profile of a poinsettia plant.

38. A database comprising the profiles of poinsettia cultivars, wherein the profile of each cultivar comprises the number of restriction fragments possessed by the cultivar and the identity of the restriction fragment, and wherein the restriction fragments are selected from the group

of fragments that have a sequence that includes a sequence selected from the group consisting of **SEQ ID NOS**: **12, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**.

39. The database of Claim 38, wherein the database is stored in a computer.

40. The database of Claim 38, wherein the database is stored in computer-readable storage media.

41. A method of identifying a plant cultivar, comprising:

obtaining a DNA fingerprint of the genomic DNA of the plant, wherein the fingerprint is a set of amplified restriction fragments, and wherein each fragment comprises a DNA sequence that includes a sequence selected from the group consisting of homologs of **SEQ ID NO:1** to **SEQ ID NO:46**; and then

comparing the fingerprint of (a) with a fingerprint comprising a set of amplified restriction fragments of the genomic DNA of a known plant cultivar, wherein each fragment comprises a DNA sequence that includes a sequence selected from the group consisting of homologs of **SEQ ID NO:1** to **SEQ ID NO:46**;

wherein the plant cultivar is a representative of the known plant cultivar if the fingerprint of the plant and the fingerprint of the known plant cultivar have the same complement of polymorphic bands.

42. The method according to Claim 41, wherein the plant cultivar is selected from the group consisting of poinsettia, begonias, impatiens, roses, geraniums, and chrysanthemums.

43. The method according to Claim 41, wherein the DNA fingerprint of the genomic DNA is of a poinsettia plant.

44. The method according to Claim 41, wherein the DNA fingerprint of the genomic DNA is obtained by AFLP, RFLP, AP-PCR, DAF, ASAP, or SSR analysis.

45. The method according to Claim 44, wherein the DNA fingerprint is obtained by AFLP analysis.

46. The method according to Claim 45, wherein the AFLP analysis is carried out by first digesting the genomic DNA with a restriction enzyme that has a tetranucleotide recognition site and a restriction enzyme that has a hexanucleotide recognition site.

47. The method according to Claim 46, wherein the restriction enzyme that has a tetranucleotide recognition site is *Mse*I, and the restriction enzyme that has a hexanucleotide recognition site is *Eco*RI.

48. The method according to Claim 45, wherein the AFLP analysis is carried out using primers that include DNA sequences selected from the group consisting of **SEQ ID NO:47, SEQ ID NO: 48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53** and **SEQ ID NO:54.**

49. The method according to Claim 45, wherein the AFLP analysis is carried out using eight primer pairs, and wherein the eight primer pairs include primers of the sequence of **SEQ ID NO:47** and **SEQ ID NO:51**; **SEQ ID NO:47** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:51**; **SEQ ID NO: 48** and **SEQ ID NO:52**; **SEQ ID NO: 48** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:54**; **SEQ ID NO:49** and **SEQ ID NO:50**; or **SEQ ID NO:49** and **SEQ ID NO:51.**

50. The method of Claim 41, wherein the fingerprint of the genomic DNA of a poinsettia plant is used to generate a profile of the poinsettia plant, wherein the profile comprises the number of restriction fragments that correspond to DNA sequences that include the DNA sequences **SEQ ID NOS**: **12, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 27, 30, 34, 35, 36, 37, 39,**

**42** and **44**, and the identity of the fragments; and wherein (b) comprises comparing the profile of the poinsettia plant to a profile generated from the fingerprint of the known poinsettia cultivar, wherein the profile of the known poinsettia cultivar comprises the number of restriction fragments that correspond to a DNA sequences that include the DNA sequences **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of the fragments.

51. The method of Claim 50, wherein the profile of the known poinsettia cultivar is stored in a database comprising profiles of known poinsettia cultivars, and wherein the profiles of the known poinsettia cultivars comprise the number of restriction fragments that correspond to DNA sequences that include the DNA sequences **SEQ ID NOS**: **12, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**, and the identity of the fragments.

52. The method of Claim 51, wherein the comparison between the profile of the poinsettia plant and the known poinsettia cultivar is carried out by a computer.

53. A method of generating a profile of a plant, wherein the profile comprises the number of amplified restriction fragments having a sequence that includes the sequence selected from the group consisting of **SEQ ID NO:1** to **SEQ ID NO:46**, and the identity of each fragment, comprising:

(a) obtaining a DNA fingerprint of the genomic DNA of the plant, wherein the fingerprint is a set of amplified restriction fragments, and wherein each fragment comprises a DNA sequence that includes a DNA sequence selected from the group consisting of **SEQ ID NO:1** to **SEQ ID NO:46**;

(b) identifying the amplified restriction fragments having a sequence that includes a sequence selected from the group consisting of **SEQ ID NO:1** to **SEQ ID NO:46** in the fingerprint; and

(c) recording the amplified restriction fragments having a sequence that includes a sequence selected from the group consisting of **SEQ ID NO:1** to **SEQ ID NO:46**, and the identity of each fragment.

54. The method according to Claim 53, wherein the DNA fingerprint of the genomic DNA of the plant is obtained by AFLP analysis.

55. The method according to Claim 54, wherein the AFLP analysis is carried out by first digesting the genomic DNA with a restriction enzyme that has a tetranucleotide recognition site and a restriction enzyme that has a hexanucleotide recognition site.

56. The method according to Claim 55, wherein the restriction enzyme that has a tetranucleotide recognition site is *Mse*I, and the restriction enzyme that has a hexanucleotide recognition site is *Eco*RI.

57. The method according to Claim 54, wherein the AFLP analysis is carried out using primers that include sequences selected from the group consisting of **SEQ ID NO:47, SEQ ID NO: 48, SEQ ID NO:49, SEQ ID NO:50, SEQ ID NO:51, SEQ ID NO:52, SEQ ID NO:53** and **SEQ ID NO:54.**

58. The method according to Claim 54, wherein the AFLP analysis is carried out using eight primer pairs, and wherein the eight primer pairs include primers of the sequence of **SEQ ID NO:47** and **SEQ ID NO:51**; **SEQ ID NO:47** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:51**; **SEQ ID NO: 48** and **SEQ ID NO:52**; **SEQ ID NO: 48** and **SEQ ID NO:53**; **SEQ ID NO: 48** and **SEQ ID NO:54**; **SEQ ID NO:49** and **SEQ ID NO:50**; and **SEQ ID NO:49** and **SEQ ID NO:51.**

59. The method according to Claim 53, wherein the profile is recorded into a database comprising at least one other profile of a plant.

60. A database comprising the profiles of cultivars, wherein the profile of each cultivar comprises the number of restriction fragments possessed by the cultivar and the identity of the restriction fragment, and wherein the restriction fragments are selected from the group of fragments

that have a sequence that includes a sequence selected from the group consisting of **SEQ ID NO:1** to **SEQ ID NO:46**.

61. The database of Claim 60, wherein the database is stored in a computer.

62. The database of Claim 60, wherein the database is stored in computer-readable storage media.

63. A method of determining whether a poinsettia plant is a representative of a known poinsettia cultivar, comprising:

(a) obtaining a DNA fingerprint of the genomic DNA of a poinsettia plant by AFLP analysis; and then

(b) comparing the fingerprint of (a) with a fingerprint of the genomic DNA of the known poinsettia cultivar;

wherein the poinsettia plant is a representative of the known poinsettia cultivar if the fingerprint of the poinsettia plant and the fingerprint of the known poinsettia cultivar have the same complement of polymorphic bands.

64. The method according to Claim 63, wherein the DNA fingerprint of the genomic DNA is a set of amplified restriction fragments, and each fragment comprises a DNA sequence that includes a DNA sequence selected from the group consisting of **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44**.

65. A method for choosing restriction fragments to be amplified in AFLP analysis of plants comprising the step of identifying sequences that contain homologs of **SEQ ID NOS**: **12**, **15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25**, **27**, **30**, **34, 35, 36, 37**, **39**, **42** and **44** in plants other than poinsettia.

66. A method of choosing primers for use in AFLP analysis of poinsettias, comprising the step of selecting primers capable of amplifying polymorphisms related to cultivar diversity.

67. A method of selecting primer pairs for use in AFLP analysis of poinsettias, comprising the steps of

(a) amplifying genomic DNA of multiple cultivars using AFLP, wherein multiple primer pairs are used in the AFLP reactions;

(b) separating the amplification products of (a) using gel electrophoresis, wherein a band in the gel represents an amplified fragment of genomic DNA;

(c) identifying amplification fragments whose bands in the gel are present in a plurality of cultivars; and then

(d) selecting the primer pairs that successfully amplified fragments that do not exhibit intracultivar variation.

68. A method of building a database of poinsettia cultivar profiles, comprising the steps of:

generating a profile of a poinsettia cultivar;

storing the profile on a computer-readable storage media; and

adding addition profiles of poinsettia cultivars to the database as they are generated.

69. A method of distinguishing a poinsettia cultivar from a known poinsettia cultivar, comprising:

obtaining a DNA fingerprint of the genomic DNA of a poinsettia plant by AFLP analysis and then;

comparing the fingerprint of (a) with a fingerprint of the genomic DNA of the known poinsettia cultivar;

wherein the poinsettia plant is not a representative of the known poinsettia cultivar if the fingerprint of the poinsettia plant and the fingerprint of the known poinsettia cultivar are dissimilar.